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# Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study

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**Abstract**

Early-onset conduct problems (CP) are a key predictor of adult criminality and poor mental health. While previous studies suggest that both genetic and environmental risks play an important role in the development of early-onset CP, little is known about potential biological processes underlying these associations. In this study, we examined prospective associations between DNA methylation (cord blood at birth) and trajectories of CP (4-13yrs), using data drawn from the Avon Longitudinal Study of Parents and Children (ALSPAC). Methylomic variation at seven loci across the genome (FDR<0.05) differentiated children who go on to develop early-onset ($n$ = 174) vs low ($n$ = 86) CP, including sites in the vicinity of *MGLL* (involved in endocannabinoid signaling and pain perception). Sub-threshold associations in the vicinity of three candidate genes for CP (*MAOA*, *BDNF*, and *FKBP5*) were also identified. Within the early-onset CP group, methylation levels of the identified sites did not distinguish children who will go on to persist vs desist in CP behavior over time. Overall, we found that several of the identified sites correlated with prenatal exposures, and none were linked to known genetic mQTLs. Findings contribute to a better understanding of epigenetic patterns associated with early-onset CP.

**Keywords**: DNA Methylation; genome-wide; ALSPAC; conduct problems; risk exposure

## Introduction

Conduct problems (CP; e.g. fighting, stealing) are a major public health concern and a leading cause of youth treatment referral (Bywater, 2012). CP youth engage in antisocial and disruptive behaviors that result in significant distress to victims, impairment of life opportunities and economic burden on judicial, healthcare and social welfare services (Colman et al., 2009). In particular, an early-onset of CP (at or before the age of 10) designates a high-risk group of children, who show more severe and recidivistic patterns of antisocial behavior, higher levels of comorbid psychopathology (E. D. Barker, Oliver, & Maughan, 2010), increased risk for poor adult outcomes (Fergusson, John Horwood, & Ridder, 2005; Odgers et al., 2007), and who account for the majority of criminal offences within a given community (David P. Farrington, 2001). Consequently, early-onset CP are recognized as an important target for prevention and intervention efforts.

Like most complex phenotypes, early-onset CP are thought to result from the developmentally dynamic interplay of genetic and environmental influences. Studies have shown that the heritability of early-onset CP is moderate to high (~50-80%, see Barker, Cecil, Walton & Meehan, in press, for a review) and that this genetic vulnerability interacts with environmental risk exposure (e.g. Jaffee et al., 2005). Indeed, exposure to adversity during pregnancy (e.g. maternal smoking, stress and psychopathology) as well as the postnatal years (e.g. maltreatment, poverty) is frequent among this group of children, and thought to play an important role in the development and persistence of CP behavior (E. D. Barker & Maughan, 2009; T. E. Moffitt, 2006; Odgers et al., 2007; Odgers et al., 2008). Yet, little is known about the biological mechanisms through which these influences confer increased risk for early-onset CP.

In recent years, DNA methylation – an epigenetic mechanism that regulates gene expression (Jaenisch & Bird, 2003) – has emerged as a potential mechanism underlying gene-environment interplay and disease susceptibility across the lifespan. Specifically, studies have shown that (i) DNAm patterns are under significant genetic control – as evidenced by the discovery of a large number of methylation quantitative trait loci (mQTL; Gaunt et al., 2016; Jones, Fejes, & Kobor, 2013); and (ii) DNAm is also sensitive to environmental influences (McGowan & Roth, 2015), including numerous nutritional, chemical, physical, and psychosocial exposures occurring in utero (e.g. Monk, Spicer, & Champagne, 2012; Richmond et al., 2015; Tobi et al., 2014) and postnatally (Lutz & Turecki, 2014; Szyf & Bick, 2013; Tyrka et al., 2015). In turn, DNAm patterns have been shown to play a central role in neurobiological and developmental processes (e.g. neurogenesis, synaptic plasticity,

learning and memory; Murgatroyd & Spengler, 2011) and aberrations in DNAm have been implicated in a range of negative outcomes, including childhood psychopathology and stress-related psychiatric disorders (Klengel, Pape, Binder, & Mehta, 2014; van Mil et al., 2014; Weder et al., 2014). Consequently, it has been suggested that DNAm may represent a molecular pathway through which environmental exposures become translated into phenotypic variation, conferring increased susceptibility to mental and physical health problems (Kofink, Boks, Timmers, & Kas, 2013; Lewis & Olive, 2014).

For example, experimental studies in animals have shown that exposure to early adversity (e.g. prenatal stress, low postnatal care) can cause alterations in offspring DNAm (e.g. in HPA-axis genes), driving differences in the offspring's behavioral response to future stressors (Weaver et al., 2004; Turecki & Meaney, 2016). Indeed, because DNAm marks can be passed on during cell division (and in some cases across generations), they can lead to long-term programming of gene expression, with downstream effects on stress sensitivity, behavior and disease risk (Rodgers & Bale, 2011; Zannas & West, 2014). In the context of CP, epigenetic alterations may thus represent a mechanism through which genetic and environmental factors intersect, influencing developmental trajectories of childhood aggression and antisocial behavior (Tremblay & Szyf, 2010).

So far, only a handful of studies in humans have examined associations between DNAm and CP-related phenotypes. Of these, the majority have been carried out by a research group comparing patterns of DNAm (extracted from peripheral blood samples collected at age 26-28) between adult males with a childhood history of chronic physical aggression (ages 6-15) vs controls who maintained low levels of physical aggression during the same time period, based on data from a longitudinal cohort (Booij et al., 2010; Guillemin et al., 2014; Provençal et al., 2013; Provençal et al., 2014; Wang et al., 2012). Using this case-control design, these studies reported that childhood aggression associated with (i) higher levels of *SLC6A4* promoter methylation and lower in vivo levels of brain serotonin synthesis (Booij et al., 2010; Wang et al., 2012); (ii) DNAm levels in a set of genes involved in cytokine function and inflammation (Provençal et al., 2013); and (iii) across a large number of gene promoter regions in an epigenome-wide scan (Provençal et al., 2014) – a finding that was later extended to a small sample of adult females as well (Guillemin et al., 2014). Another set of studies based on a sample of antisocial boys diagnosed with oppositional defiant disorder or conduct disorder (4-16yrs) have also documented an association between severity of callous-unemotional traits (CU; e.g. low capacity for empathy, lack of guilt, shallow affect) and DNAm levels (obtained from peripheral blood) across several candidate genes,

including lower DNAm of the Serotonin 1B Receptor gene (*HTR1B*; Moul, Dobson-Stone, Brennan, Hawes, & Dadds, 2015), and higher DNAm of the Oxytocin Receptor gene (*OXTR*; Dadds et al., 2014) – which in turn related to lower circulating oxytocin levels.

Despite these promising findings, research to date has been limited in a number of important ways. First, no study to our knowledge has specifically investigated DNAm patterns associated with early-onset CP, which designates a subgroup of children at high risk for negative adult outcomes. Second, the available research has been primarily cross-sectional or retrospective with regards to DNAm (i.e. associating behavioral phenotypes in childhood to DNAm later in development). As such, it is currently unclear whether observed alterations in DNAm patterns represent a *risk factor* for and/or a *consequence* of conduct problems. In other words, it has not been possible to establish whether DNAm is a prospective risk for CP, or alternatively, the biological correlate of a chronic antisocial lifestyle. Third, there is a lack of studies integrating measures of the environment, which has precluded the possibility of assessing the epigenome in relation to *both* risk exposure and psychiatric phenotypes.

To address the above gaps, research from our group has begun to assess prospective associations between environmental risks, DNAm at repeated time points (birth, childhood) and CP-related outcomes, using data from the Avon Longitudinal Study of Parents and Children (ALSPAC; Fraser et al., 2013). For example, in children with early-onset CP and low internalizing problems, we found that DNAm levels in the promoter region *OXTR* at birth (but not at later points in childhood) associated with higher risk exposure in utero, reduced experience of victimization during childhood (i.e. indicative of an 'evocative epigenetic-environment correlation') and more severe CU traits at age 13 (Cecil et al., 2014). Also in early-onset CP, we found that a sugar- and fat-rich diet during pregnancy prospectively associated with higher DNAm of the Intrauterine Growth Factor Gene 2 (*IGF2*) at birth (but not during childhood), which, in turn, associated with more severe co-occurring ADHD symptoms (Rijslasdaam et al., 2016a). The temporal specificity around birth observed across these and other studies (e.g. Cecil et al., 2016; Walton et al., 2016) may reflect a number of factors, including large-scale variability in DNAm patterns across developmental eras (Gaunt et al., 2016), differences between the tissues examined at each time point (i.e. cord blood at birth vs whole blood in childhood), as well as the influence of developmentally-specific genetic effects on symptom trajectories (e.g. Pingault, Rijsdijk, Zheng, Plomin & Viding, 2015). Additionally, findings may lend support for the developmental origins of health and disease hypothesis (DOHaD; D. J. Barker, 2007; Nigg, 2016), whereby

methylation changes at birth may represent a more reliable proxy for intra-uterine risk exposures (compared to DNAm in childhood), and associated perturbations in fetal development. However, the extent to which DNAm patterns across the genome at birth may prospectively associate with an early-onset of CP has yet to be examined.

In addition to advancing knowledge of potential biological differences between children with early-onset vs low CP, the study of DNAm may also help us to better understand why early-onset children themselves show considerable heterogeneity in their developmental trajectories of CP. Indeed, studies have found that – despite being considered a high-risk group as a whole - less than 50% of children with an early-onset of CP will actually continue to exhibit these problems into adolescence (i.e. early-onset persisting trajectory, EOP), while the rest will remit to near-typical levels of CP (i.e. childhood-limited trajectory, CL; E. D. Barker & Maughan, 2009; Odgers et al., 2008). This heterogeneity poses a challenge for accurate diagnostic screening, clinical classification and treatment formulation, as well as raising important questions about what factors may underlie these increasingly divergent trajectories of CP within early-onset children (i.e. in line with the concept of multifinality; Cicchetti & Rogosch, 1996). So far, evidence regarding early-life predictors of EOP vs CL trajectories has been somewhat mixed (see Moffitt et al., 2008, for a review), but generally suggests that the difference may be more quantitative than qualitative, with pre- and postnatal risk exposures found to be particularly high for EOP children, compared to their CL peers (i.e. EOP>CL>Low CP; E. D. Barker & Maughan, 2009). However, it is currently unknown whether such a 'graded' difference on the same risk factors may also **exist** at a biological level. The analysis of DNAm patterns between early-onsets who follow different developmental trajectories of CP (i.e. EOP vs CL), may therefore help to refine the phenotype and contribute to a better understanding of heterogeneity within this high-risk group of children.

**The present study**

In light of the above research gaps, we made use of data from the ALSPAC cohort spanning pregnancy to late childhood to address three key aims. First, we examined whether DNAm patterns at birth (measured at >450,000 sites across the genome) prospectively differentiate children who will go on to develop early-onset ($n$ = 174) vs low CP ($n$ = 86). Second, to explore heterogeneity in CP trajectories within the early-onset group, we tested whether these DNAm patterns further distinguish between children who will persist (EOP; $n$ = 91) vs desist (CL; $n$ = 83) in conduct problems over time. Third, we investigated potential

genetic and environmental influences associated with the identified DNAm sites, including known genetic mQTLs and measures of prenatal adversity that have been previously linked to early-onset CP (e.g. maternal diet, smoking, and exposure to stressful events).

## Methods

### Sample

The *Epigenetic Pathways to Conduct Problems Study* consists of a subsample of youth (*n*=321; 50% female) drawn from the *Avon Longitudinal Study of Parents and Children* (ALSPAC) and partially overlapping with a larger study of DNA methylation, the Accessible Resource for Integrated Epigenomics Studies (ARIES, www.ariesepigenomics.org.uk; Relton et al., 2015). Specifically, children were included if they (i) have available measures of DNAm at two or more time points and (ii) follow previously established trajectories of conduct problems between 4 and 13 years of age (see measures section below; E. D. Barker & Maughan, 2009). Children in this study were white Caucasian (six removed from analyses due to missing ethnicity data).

ALSPAC is an ongoing epidemiological study of 14,541 pregnant women resident in Avon, UK with expected dates of delivery 1st April 1991 to 31st December 1992. Of these initial pregnancies, there was a total of 14,676 fetuses, resulting in 14,062 live births and 13,988 children who were alive at 1 year of age (Fraser et al., 2013). When compared to 1991 National Census Data, the ALSPAC sample was found to be broadly similar to the UK population as a whole (Boyd et al., 2013). The study website contains details of all the data that is available: http://www.bris.ac.uk/alspac/researchers/data-access/data-dictionary. Ethical approval for the study was obtained from the ALSPAC Law and Ethics Committee and the Local Research Ethics Committees.

### Measures

#### *Conduct Problems*

CP trajectories were previously identified and validated in the whole ALSPAC sample using growth mixture models based on repeated measures of the Strengths and Difficulties Questionnaire 'conduct problems' subscale (ages 4,7,8,10,12,13; SDQ; Goodman, 2001), with boys and girls modeled in the same trajectories (E. D. Barker & Maughan, 2009). The original analysis identified four CP trajectories: (i) an *early-onset persistent* (EOP; 9%) group of children, who show high levels of CP early on and remain high across time; (ii) a *childhood-limited* (CL; 15%) group who also show an early-onset of CP, but desist around

adolescence; (iii) an *adolescent-onset* group who only show CP behaviors later on (AO; 12%); and (iv) a *low* CP group, who maintain low levels of CP throughout (Low CP; 64%). The percentage of youth identified in the CP trajectories in ALSPAC is consistent with reported prevalence estimates in the general population (4-20%; Egger & Angold, 2006; Kim-Cohen et al., 2003). In contrast to the overall ALSPAC sample, our epigenetic subsample featured a near equal number of youth in each trajectory, and was therefore enriched for CP (EOP: $n$ = 91, 28%; CL: $n$ = 83, 26%; AO: $n$ = 61, 19%; Low CP: $n$ = 86, 27%). In this study, early-onset CP youth were defined as youth who follow either an EOP or CL trajectory. The adolescent-onset (AO) group was excluded from the main analyses for two reasons. First, although AO and Low children appear phenotypically similar in CP levels during the developmental period under investigation, they have been shown to differ in levels of environmental risk exposure and temperamental features (Barker & Maughan, 200), so that we decided against combining AOs within the Low (i.e. typical) group. Second, we did not include AOs as a separate comparison group in the epigenome-wide analyses due to concerns over statistical power and multiple testing burden resulting from the increase in number of comparisons.

*DNA Extraction and Methylomic Profiling*

DNA was obtained from cord blood samples at birth. 500ng genomic DNA was bisulfite converted using an EZ-DNA methylation kit (Zymo Research, Orange, CA, USA) and DNAm quantified using the Illumina HumanMethylation450 BeadChip (450K array; Illumina, USA) with arrays scanned using an Illumina iScan (software version 3.3.28). The Illumina 450K array comprises >485,000 probes, each quantifying DNAm at a specific CpG site, covering 99% of Reference Sequence (RefSeq) genes, with an average of 17 CpG sites per gene region (distributed across promoter, 5'UTR, first exon, gene body and 3'UTR regions). The BeadChip covers 96% of CpG islands, with additional coverage in island shores and their flanking regions. Initial quality control of data generated was conducted using GenomeStudio (version 2011.1) to determine the status of staining, extension, hybridization, target removal, bisulfite conversion, specificity, non-polymorphic and negative controls. Furthermore, multiple checks for sample mismatch were carried out to ascertain that all cord blood samples in the study reflected infant DNA as opposed to maternal DNA. Specifically, samples were checked by calculating concordance with (i) GWA data from the same participants, (ii) SNP probes on the Illumina 450k array across mother and child, and (iii) sex. Data were quantile normalized using the *dasen* function as part of the *wateRmelon*

package (wateRmelon_1.0.3; Pidsley et al., 2013) within the R statistical analysis environment and batch corrected using the ComBat package (Johnson, Li, & Rabinovic, 2007). Probes previously reported to hybridize to multiple genomic regions or containing a SNP at the single base extension site were removed from subsequent analyses (Chen et al., 2013; Price et al., 2013), in addition to the 65 SNPs used for sample identification on the array (total probes removed 72,067). For each probe, DNAm levels were indexed by beta values – i.e. the ratio of methylated signal divided by the sum of the methylated and unmethylated signal ($M/M+U$).

*Prenatal environment*

Multiple environmental influences were included that have been previously linked to early-onset CP, including maternal prenatal diet, smoking, alcohol use and exposure to stressful events (E. D. Barker & Maughan, 2009). Information on dietary patterns was drawn from maternal ratings of the Food Frequency Questionnaire at 32 week gestation, where factor scores of 'healthy' (i.e. high on fish, non-meat protein and vegetables) and 'unhealthy' (i.e. high on processed and junk food) diet were extracted using confirmatory factor analysis, both of which showed acceptable model fit (for full details, see E. D. Barker, Kirkham, Ng, & Jensen, 2013). Maternal smoking and alcohol use during the first trimester of pregnancy were measured via maternal ratings, using a yes/no binary variable for smoking, and a 4-point scale for alcohol use ('never' to 'daily'). With regards to stress exposure, we included cumulative risk scores of prenatal (18 to 32 weeks) adversity, based on 56 dichotomous items from the Life Events inventory (adapted in ALSPAC based on the work of Brown et al., 1973 and Barnett et al.,1983) and the Family Adversity Index (Wolke, Steer & Bowen, 2004). Briefly, items were organized into four conceptually distinct but related risk domains, and summed to create the following cumulative scores: (i) life events (22 items; e.g. death in family, accident); (ii) contextual risks (16 items; e.g. poor housing, financial problems); (iii) maternal risks (10 items; e.g. psychopathology, criminal behavior); and (iv) interpersonal risks (8 items; e.g. partner abuse, family conflict). The full list of items contained in these cumulative scores is provided in online supplement OS1, and further information is available elsewhere (Cecil et al., 2014b; Rijlaarsdam et al., 2016b).

Statistical Analyses

All analyses were performed within R (version 3.0.1; R Core Team, 2014) on DNAm data regressed for sex and cell-type proportions (CD8 T lymphocytes, CD4 T lymphocytes, natural killer cells, B lymphocytes, monocytes), estimated using the reference-based approach detailed in Houseman et al. (2012).

*Step 1: Are there differences in neonatal patterns of DNAm between children who go on to develop early-onset vs low CP?*

First, a methylome-wide association analysis was performed using the CpGAssoc package (Barfield, Kilaru, Smith, & Conneely, 2012) to identify DNAm sites at birth that differentiate children who go on to develop early-onset (i.e. EOP and CL) vs low CP. False discovery rate (FDR) correction was implemented across all probes (i.e. genome-wide significance threshold set at $q < 0.05$). Effect sizes were calculated and interpreted following Cohen's guidelines, where an effect of 0.20 represents a small effect, and effect of 0.50 is a medium effect and an effect of 0.80 is a large effect (Cohen, 1988).

Genome-wide significant loci were then uploaded to the UCSC genome browser (GRCh37/hg19 assembly; Kent et al., 2002) to explore their potential functional relevance, by comparing their genomic location to that of key regulatory elements recorded in the Encyclopedia of DNA Elements (ENCODE) database (http://genome.ucsc.edu/ENCODE/). These included (i) *transcription factor binding sites*, i.e. DNA regions where one or more specific proteins responsible for regulating transcription bind to (data generated on 161 transcription factors in 91 cell types via ChIP-seq); (ii) *DNase I hypersensitivity clusters*, which tend to coincide with regulatory regions of the gene and indicate an open chromatin state that facilitates transcription (based on data from 125 cell types), and (iii) *histone marks*, i.e. chemical modifications that influence how tightly packaged the DNA is around histone protein, thereby regulating how accessible DNA is for transcription (data available for seven cell types; however, given that DNAm patterns can be tissue specific, we only selected here the three cell-types that are most relevant to cord blood; i.e. blood [GM12878, K562] and umbilical vein endothelial [HUVEC] cells). To identify enriched biological pathways, we also analyzed probes that were significant at $p<0.001$ using an optimized gene ontology method that corrects for multiple potential confounds, including background probe distribution and gene size (see **OS2**).

*Step 2: Within the early-onset group, do these DNAm sites also differentiate children who will persist vs desist in CP over time?*

As a second step, we examined whether the identified DNAm sites may help to explain heterogeneity in developmental trajectories within the early-onset CP group. Specifically, we used one-way Analysis of Covariance (ANCOVA) models to test whether DNAm levels across the sites identified in Step 1 also differentiate early-onsets who will go on to follow a persisting (i.e. EOP) vs desisting (i.e. CL) trajectory of CP behaviour over time, controlling for sex and cell-type proportions.

*Step 3: Are the identified DNAm sites associated with genetic and environmental factors?* As a final step, we explored potential genetic and environmental factors that may influence the DNAm sites associated with early-onset CP (i.e. identified in Step 1). As our sample was underpowered to directly examine genetic polymorphisms (i.e. SNPs) affecting DNAm, we used the mQTLdb resource (http://www.mqtldb.org/) to search for known methylation quantitative trait loci (mQTLs) associated with our DNAm sites of interest. The mQTLdb database contains the results of a large-scale study based on the ARIES sample in ALSPAC (from which our subsample is derived), characterizing genome-wide significant *cis* effects (i.e. SNP within ±1000 base pairs of the DNAm site) and *trans* effects (i.e. ±1 million base pairs) on DNAm levels across Illumina 450k probes at five different life stages, including cord blood DNAm at birth (Gaunt et al., 2016). Here, we searched for mQTLs based on results from the conditional Genome-wide Complex Trait Analysis (GCTA), which was used to identify mQTLs with the most representative, independent effect on each DNAm site in order to account for linkage disequilibrium (Gaunt et al., 2016). With regards to environmental influences, we examined associations between DNAm levels in the identified sites and prenatal exposures (i.e. maternal diet, smoking, alcohol use and stressful events) using Pearson's bivariate correlations. Again, the significance threshold was set at an FDR-corrected level of $q<0.05$ to adjust for multiple comparisons.

## Results

Neonatal DNA methylation and early-onset CP

The Q-Q plot and Manhattan plot for the epigenome-wide association analysis at birth are displayed in **Figure 1 (A-B)**. **Table 1** shows the seven differentially methylated sites (q-value < 0.05) between early-onset vs low CP groups, as identified via our genome-wide analysis. Group differences were medium to large in effect size based on Cohen's guidelines

($d$ = 0.66 – 0.84), and ranged from 4% to 8% in terms of mean DNAm difference. Of note, all seven sites remained differentially methylated after additionally adjusting for gestational age. DNAm levels across these sites were all significantly inter-correlated (both positive and negative correlations observed; see **OS3**). Three of the sites had genic annotations (**Figure 1C**): (i) cg02503763, located in the promoter regulatory region of *MGLL*, a gene implicated in endocannabinoid signaling and nociperception (Iwasaki, Ishiguro, Higuchi, Onaivi, & Arinami, 2007); (ii) cg21579239, annotated to the 5'UTR region of *TTBK2*, a gene involved in tau protein phosphorylation, of which mutations have been linked to neurodegenerative disorders (Liao, Yang, Weng, Kuo, & Chang, 2015); and (iii) cg16006965, located in the promoter regulatory region of *GCET2*, a gene implicated in immune function (Pan et al., 2007). The other four differentially methylated sites identified at birth were distal to annotated transcripts (see **OS4** for boxplots): cg12628061 located between *AK127270* (-407kb) and *PPAP2B* (-507kb), cg02131674 located closest to *BASP1* (-123kb), cg15384400 located between *ARAP2* (-12kb) and *DTHD1* (+26kb), and cg07128473 located between *TRPS1* (-210kb) and *EIF3H* (+876kb). In all cases – except for probe cg15384400 – methylation of these sites was *lower* in the early-onset vs low CP groups. These seven sites were then viewed in Genome Browser for functional characterization, based on ENCODE data on regulatory elements. Four of the DNAm loci coincided with transcription factor binding sites, including $MGLL_{cg02503763}$ and $GCET2_{cg16006965}$, and implicated a number of shared transcription factors, including MAX (4/4 loci), POLR2A, RUNX3 and EP300 (3/4 loci). The majority of DNAm sites also overlapped with histone marks (6/7 loci) and DNAse I hypersensitive clusters (4/7 loci), suggesting that they are located in genomic regions that are likely to play regulatory roles in transcription. Gene ontology analysis ($n_{probes}$ = 1101; $n_{genes}$ = 758) further indicated that DNAm sites (at birth) that differentiate between CP groups are annotated to genes involved in a range of biological processes, including regulation of fat cell differentiation and immune system process, response to epinephrine and wounding, as well as forebrain generation of neurons and CNS neuron differentiation (2.95E-15 <p< 6.66E-05, **Figure 1D**). GO results for the top 20 enriched biological pathways (including those displayed in Figure 1D) are provided in **OS5.**

********** **Table 1** **********

********** **Figure 1** **********

In light of the above findings, we conducted two follow-up analyses to further investigate the relationship between DNAm at birth and early-onset CP.

*Methylomic variation in MGLL, TTBK2 and GCET2.*

Our genome-wide analyses indicated that three of the seven sites identified as differentiating early-onset vs low CP children were annotated to genes, including *MGLL*, *TTBK2* and *GCET2* (one site each). As an additional step, we examined whether any other probes in the vicinity of these genes associated with early-onset CP at a nominal level. While none of the other probes in *TTBK2* ($n_{total}$ = 10 probes) or *GCET2* ($n_{total}$ = 19 probes) associated with early-onset vs low CP ($p > 0.05$), four additional probes in *MGLL* were differentially methylated between groups, including another probe in the TSS1500 region (cg02116612; $p$ = 1.95E-05; significant at gene-level Bonferroni correction: 0.05/26 total annotated probes = 0.002) and three probes in the gene body region (cg14476212, $p$ = 0.028; cg10319942, $p$ = 0.034*;* and cg15694422, $p$ = 0.048). The location of these probes and their relationship to ENCODE regulatory elements is displayed in **Figure 2** (for more detailed information, see **OS6)**. Of note, two of these additional probes correlated significantly with the genome-wide significant site $MGLL_{cg02503763}$ – including a stronger association with the most proximal probe in the TSS1500 region (cg02116612; $r$ = 0.46, $p$ = 6.04E-15) and a weaker association with one of the probes in the gene body (cg10319942; $r$ = 0.15, $p$ = 0.01).

********** **Figure 2** **********

*Methylomic variation in candidate genes for conduct problems.*

As shown in **Table 1**, none of the genome-wide significant loci identified resided in 'traditional' candidate genes for CP. In order to maximise comparability with existing molecular studies, we carried out a follow-up analysis to investigate DNAm variation in the vicinity of genes that have been previously implicated in CP-relevant phenotypes. The selection of candidate genes was informed by a recent systematic review (Waltes, Chiocchetti, & Freitag, 2015) and meta-analysis (Pappa et al., 2015) of genetic influences on aggression. Specifically, we selected a total of 15 genes ($n_{total}$ = 387 probes), across (i) dopaminergic (*MAOA* [14 probes], *COMT* [22 probes], *SLC6A3* [52 probes],*DRD2* [22 probes], *DRD4* [21 probes]); (ii) serotonergic (*SLC6A4* [14 probes], *HTR1A* [14 probes], *HTR2A* [25 probes], *TPH1* [4 probes], *TPH2* [18 probes]); and (iii) neuroendocrine and neurodevelopmental pathways (*NR3C1* [35 probes], *FKBP5* [32 probes], *AVP* [14 probes], *OXTR* [17 probes], *BDNF* [73 probes]). As done by Weder et al. (2014), we used a gene-level

Bonferroni correction for these hypothesis-driven analyses, correcting for the total number of probes within each gene.

In total, 12% of probes were differentially methylated between groups at a nominal significance threshold ($p<0.05$), with at least one probe associating with early-onset CP for each gene (see **OS7**). However, only 4 of these loci survived gene-level Bonferroni-correction (see **Table 2**), including sites annotated to *BDNF* (cg01225698, cg18354203), *FKBP5* (cg07061368) and the *MAOA* promoter region (i.e. TSS200; cg05443523). Effect sizes for these loci were small ($d$ = 0.44-0.49), and mean group DNAm differences ranged from 1% to 3%. Based on ENCODE data, all four probes coincided with transcription factor binding sites and histone marks, with two of the probes additionally coinciding with DNase I hypersensitivity clusters. As with the loci identified via our epigenome-wide analysis, these four probes remained significantly associated with CP trajectory after controlling for gestational age.

********** **Table 2** **********

Comparison of top DNAm probes between early-onsets who persist vs desist in CP

Within the early-onset CP group, none of the DNAm sites identified in the previous step (i.e. 7 FDR-corrected genome-wide significant loci and 4 Bonferroni-corrected loci from the candidate gene follow-up analyses) were found to differentiate children who will go on to follow a persisting vs desisting trajectory of conduct problems over time ($p > 0.05$, see **OS8** for full results). This lack of differences suggest that, while methylomic variation at birth prospectively associates with an early-onset of CP (i.e. distinguishing between high vs low CP early in childhood), this variation is not likely to contribute towards heterogeneity in developmental trajectories of conduct problems observed within early-onset children.

Potential relevance of genetic and in utero environmental influences on the identified DNAm sites

The 11 DNAm sites associated with early-onset CP were carried forward to explore associations with potential genetic and environmental influences. Based on mQTLdb search, we found that none of the identified loci were associated with *cis* or *trans* mQTLs, suggesting that DNAm levels across these sites are not likely to be heavily influenced by known genetic polymorphisms. Bivariate correlations between the DNAm loci and prenatal exposures are shown in **Table 3**, controlling for sex and cell-type. Of the 11 probes examined, 7 were nominally correlated with one or more exposures ($p < 0.05$), but none of these associations

remained significant after multiple correction ($q > 0.05$). The majority of associations involved maternal smoking and alcohol use during the first trimester of pregnancy. Around half of associations identified remained significant after additionally controlling for all other prenatal exposures (i.e. unique association, see **Table 3**).

********** **Table 3** **********

## Discussion

This is the first study to investigate the epigenetic landscape of early-onset conduct problems, using a prospective design. The study offers a number of strengths, including the examination of genome-wide data collected *prior* to the emergence of CP symptoms, the inclusion of the largest epigenetic CP sample to date, allowing for adequately-powered group comparisons (Tsai & Bell, 2015), as well as the integration of environmental, DNAm and phenotypic data. We highlight here three key findings: (i) methylomic variation across multiple loci at birth differentiated children who go on to develop early-onset vs low CP; (ii) DNAm levels across these loci were comparable for early-onsets who persist vs desist in CP over time; and (iii) several of the identified loci showed suggestive associations with prenatal exposures, while none were linked to known genetic mQTLs.

<u>Genome-wide findings point to the potential importance of methylomic variation at birth</u>

The use of a genome-wide, hypothesis-free approach enabled us to identify novel loci for CP, pointing to potential avenues for future investigation. Specifically, we found that seven loci at birth prospectively differentiated CP groups, showing a moderate-to-large effect size difference between children who go on to develop early-onset vs low CP. Functional characterization using ENCODE data indicated that the majority of the identified sites coincided with regulatory elements that play a key role in gene expression, including transcription factor binding sites, DNase I hypersensitivity clusters (i.e. regions of open chromatin) and histone marks. Six of the loci were significantly hypomethylated in early-onset vs low CP children, and three were annotated to genes. Of these, *MGLL* encodes a serine hydrolase that converts monoacylglycerides to free fatty acids and glycerol and acts as a major endocannabinoid metabolic enzyme (Iwasaki et al., 2007). Interestingly, previous studies have shown that *MGLL* activity associates with substance abuse (Hopfer et al., 2007), which is highly comorbid with CP (McAdams, Salekin, Marti, Lester, & Barker, 2014). Furthermore, CB1 cannabinoid receptor function (modulated indirectly by *MGLL* via 2-Arachidonoylglycerol [2-AG] activation) has been shown to mediate aggression in animal

knockout studies (Rodriguez-Arias et al., 2013). Together, these findings support a link between *MGLL* function and CP-relevant phenotypes, although more work will be needed to delineate the functional effects of *MGLL* methylation on broader endocannabinoid signaling and downstream consequences on behavior. We do note that in follow-up analyses, a number of additional DNAm sites associated with early-onset CP across the promoter region and gene body of *MGLL*, as well as coinciding with key regulatory elements, which further supports a link between epigenetic regulation of this gene and CP.

Another DNAm site that showed CP-related DNAm at birth was annotated to *TTBK2*. This gene is highly expressed in subcortical brain structures (e.g. cerebellum, hippocampus) and is involved in the phosphorylation of tau and tubulin, two key microtubule stabilization proteins that are robustly associated with multiple nervous system pathologies, including Alzheimer's disease (Liao et al., 2015). Although we are not aware of studies directly investigating the link between *TTBK2* and CP-relevant phenotypes, it is noteworthy that associations between levels of tau phosphorylation in the brain and aggressive behavior have been previously reported in patients with Alzheimer's disease (e.g., Guadagna, Esiri, Williams, & Francis, 2012). As such, it will be of interest in future to examine whether *TTBK2* methylation may contribute to early-onset CP via microtubule alterations in the brain.

The third gene identified, *GCET2*, plays a role in immune processes, including cytokine function (Pan et al., 2007). While an increasing number of studies has documented a link between inflammation and psychiatric phenotypes, including childhood aggression (e.g. Provençal et al., 2013), little is known about the function of this gene in relation to CP. It is interesting; however, that a genome-wide study recently identified *GCET2* expression levels as a potential biomarker for antidepressant treatment response (Hennings et al., 2015), pointing to a potential role of this gene in mood regulation.

<u>DNA methylation of candidate genes: Maximizing comparability with previous studies</u>

Consistent with what has been previously reported in the psychiatric epigenetic literature (e.g. Cecil, Walton, & Viding, 2015), we found that none of the DNAm sites identified via our hypothesis-free, epigenome-wide analysis were annotated to genes that are typically examined in hypothesis-driven, candidate gene studies. In order to maximize comparability with existing molecular studies, we carried out an additional analysis focusing on DNAm in the vicinity of 15 genes that have been extensively investigated in relation to CP and related phenotypes (e.g. aggression; Pappa et al., 2015; Waltes et al., 2015). It is important to note that these studies have primarily focused on genetic (as opposed to epigenetic) contributions

to CP, so that a direct test of replication was not possible. Rather, this follow-up analysis was designed to explore the potential role of these genes in early-onset CP from an epigenetic perspective. Although none of the DNAm sites annotated to candidate genes passed genome-wide correction, sub-threshold associations were identified across three genes, including *BDNF* (two probes), *MAOA* (one probe) and *FKBP5* (one probe). Of note, effect sizes were small but not trivial (>0.44), suggesting that these DNAm differences may hold relevance for understanding biological vulnerability for early-onset CP.

*BDNF* encodes for a neutrophic protein that performs a wide range of functions, including regulation of neurodevelopment, synaptic plasticity and mood. While a link between aggression and *BDNF* activity has been documented by multiple lines of evidence – including findings from genetic, knock-out, endocrine and pharmacological studies (Waltes et al., 2015) – this is the first report, to our knowledge, of an association with *BDNF* DNAm levels. The role of *MAOA* activity on aggression has also received widespread attention from both the animal and human literature, due to its key role in the degradation of amine neurotransmitters in the brain, including dopamine, norepinephrine and serotonin (Nelson & Trainor, 2007). Consistent with our findings, a recent study reported that hypermethylation of the *MAOA* promoter region (with an average DNAm difference between groups of 3% - the same as observed in the present study) was associated with antisocial personality disorder in a forensic population, as well as decreased gene expression and dysregulation of serotonin blood serum levels (Checknita et al., 2015). Interestingly, *MAOA* promoter DNAm in blood has also been shown to robustly predict *MAOA* enzymatic activity in the brain (Shumay, Logan, Volkow, & Fowler, 2012), suggesting that peripheral *MAOA* DNAm status may be a promising biomarker for functional levels in live central tissue, which is most relevant to CP. Finally, the *FKBP5* gene, which codes a co-chaperone of the glucocorticoid receptor that regulates its sensitivity, has been extensively investigated for its role in mediating stress, hormonal and immune responses to adverse experiences, particularly in the context of gene-environment interactions (Zannas & Binder, 2014). For example, *FKBP5* polymorphisms have been found to interact with childhood trauma (e.g. maltreatment) to predict a range of psychiatric outcomes, including childhood aggression (Bryushkova et al., 2016). While emerging evidence suggests that *FKBP5* methylation may mediate these observed GxE interactions (Zannas, Wiechmann, Gassen, & Binder, 2015), more work is needed to characterize its relevance to CP behaviour.

Heterogeneity in developmental trajectories within the early-onset CP group

Whereas the identified DNAm sites at birth differentiated children who develop early-onset vs low CP, these same sites did not further discriminate between early-onsets who go on to follow a persisting (i.e. EOP) vs desisting (i.e. CL) trajectory of CP into adolescence. This lack of associations may reflect a number of possibilities. For example, it is possible that, at birth, EOP and CL children may be phenotypically and biologically similar. In other words, while they may both be at increased risk for early-onset CP relative to typical children, it may not yet be possible to separate those who will persist vs desist in CP behavior over time. Given that EOP vs CL children start to diverge in levels of CP around late childhood and predict different outcomes in adulthood (David P Farrington, Gallagher, Morley, Ledger, & West, 1988; Terrie E Moffitt, Caspi, Harrington, & Milne, 2002), it will be of interest in future to extend epigenetic analyses later in development, so as to investigate whether these behavioural differences may coincide with underlying epigenetic differences. In addition, the examination of DNAm at later time points would enable one to test potential associations with postnatal environmental influences, which are likely to play an important role in the divergence between EOP and CL trajectories. It is also possible that statistically, our analyses were underpowered to examine within-group differences in DNAm patterns among the early-onset group. Larger longitudinal studies will be needed in future to enable a more fined-tuned comparison of DNAm patterns between EOP and CL children across multiple developmental periods.

Genetic and prenatal influences on DNAm patterns associated with early-onset CP

As a final step, we investigated whether DNAm loci at birth that differentiated between early-onset vs low CP children (both at the genome-wide and candidate-gene level) were also associated with potential genetic and environmental influences relevant to CP (E. D. Barker & Maughan, 2009; Salvatore & Dick, 2016). Based on findings from a large-scale study of genetic effects on DNAm (Gaunt et al., 2016), we found that none of the identified loci associated with known *cis* or *trans* mQTLs. While this suggests that the identified loci were unlikely to be heavily influenced by genetic structure, it is important to note that the heritability of DNAm patterns is greater than what can currently be explained using known mQTLs (Gaunt et al., 2016). As such, it is still possible that the identified loci may have been influenced by polygenic effects, involving many mQTL that each explain too little variance in isolation to be detected with currently available samples.

With regards to environmental influences, we identified suggestive associations between the identified DNAm sites and prenatal exposures. Of note, we found that proximal exposures (e.g. maternal smoking and alcohol use) correlated with DNAm more strongly than more distal exposures (e.g. life events). Albeit preliminary, these findings are consistent with previous studies showing that DNAm is associated with environmental influences (e.g. Lewis & Olive, 2014), with smoking-related effects, in particular, being amongst the most replicated across epigenetic studies (Gao, Jia, Zhang, Breitling, & Brenner, 2015). For example, we found that prenatal smoking correlated with hypomethylation of the *MGLL* probe, which in turn prospectively associated with early-onset CP. This is of interest given that activity of this gene has been shown to influence nicotine withdrawal in animals and humans (Muldoon et al., 2015), as well as interacting with environmental exposures to predict cannabis dependence symptoms and amygdala function (Carey et al., 2015). However, it is important to note that the associations identified in the present study were based on correlational analyses and did not survive multiple correction. Consequently, they should be interpreted with caution and considered more as well-grounded hypotheses for further examination in larger longitudinal studies.

Limitations

Findings should be interpreted in light of a number of limitations. First, because results from this study were based on DNAm collected from peripheral samples, the extent to which they may be tissue-specific is unclear. More research will be needed to assess the relevance of the identified DNAm sites to brain tissue, as well as characterizing their potential role in CP-related brain-based phenotypes. Furthermore, because we did not have access to RNA, functional characterization of the identified loci was performed using recorded ENCODE data. However, integration of transcriptomic data will mark an important step toward establishing the functional significance and downstream effects of the observed DNAm changes. Second, the current study was based on a community sample of children with relatively low rates of CP. In future, it will be important to replicate our findings in high-risk populations who show more severe externalising problems (e.g. young offenders, psychiatric inpatients). Furthermore, the use of a larger number of cases vs controls will make it possible to examine potential moderators in the relationship between DNAm and early-onset CP (e.g. sex). Finally, although we used a prospective design where DNAm was collected prior to the emergence of CP symptoms, the results from the study are correlational and cannot be taken to reflect causal pathways. As such, findings should be considered as hypothesis-generating

and in need of replication. In future, the application of advanced inference methods (e.g. two-step Mendelian randomization; Pingault, Cecil, Murray, Munafò & Viding, 2016; Relton & Davey Smith, 2012), will offer unique opportunities to establish causal relationship between prenatal environmental risk, DNAm and CP.

## Conclusion

In this study, we find that DNA methylation at multiple loci at birth prospectively associated with early-onset vs low conduct problems. These findings highlight the neonatal period as a potentially important window of biological vulnerability for conduct problems, as well as pinpointing novel potential risk markers for future investigation. Suggestive evidence of associations between the identified loci and prenatal exposures also lend preliminary support for a link between the early environment, DNA methylation and the development of early-onset conduct problems.

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**Figure legends:**

**Figure 1**. **Methylomic variation at birth prospectively associated with early-onset vs low conduct problems in childhood.** Epigenome-wide associations between DNA methylation at birth and early-onset vs low conduct problems (CP), including Q-Q plot (**A**), Manhattan plot (**B**) and scatterplots of the top 3 differentially methylated sites with genic annotations (**C**). Significantly enriched biological processes at birth are shown in (**D)**, based on gene ontology (GO) analysis of genes annotated to probes that associate with early-onset vs low CP ($p < 0.001$). Circles represent GO terms that survive FDR-correction and contain at least two genes. The X axis represents -log(10) p-values. The opacity of the circles indicates level of significance (darker = more significant). The size of the circles indicates the percentage of genes in our results for a given pathway compared to the total number of genes in the same pathway (i.e. larger size = larger %).

**Figure 2. Functional characterization of *MGLL* DNA methylation sites associated with early-onset conduct problems**. Expanded views from the UCSC genome browser of the *MGLL* gene showing the position of the DNAm sites associated with early-onset CP relative to ENCODE regulatory elements. Track numbers are displayed on the left-hand site, and represent the following **(1)** genomic positon of *MGLL* in chromosome 3; **(2)** genomic coordinates and scale; **(3)** location of all Illumina 450k probes that map onto the *MGLL* gene ($n = 26$); **(4)** location of differentially methylated probes associated with early-onset vs low conduct problems ($n = 5$). These are highlighted in blue to facilitate comparison with the regulatory elements displayed in lower tracks (track 6-8). In red is the probe that survived genome-wide correction ($MGLL_{cg02503763}$; all other probes significant at $p<0.05$); **(5)** schematic representation of the *MGLL* gene; **(6)** location of transcription factors (based on ChIP-seq data from 91 cell types), where darker shades indicate a stronger signal occupancy; **(7)** DNaseI hypersensitivity clusters (based on ChIP-seq data from 125 cell types), where darker shades also indicate a stronger signal; and **(8)** levels of enrichment of three histone marks (H3K27Ac, H3K4Me1, and H3K4Me3) across three cell-types, including blood (GM12878 [red], K562 [purple]) and umbilical vein endothelial (HUVEC [blue]) cells.

**Table 1.** DNA methylation sites at birth that differentiate early-onset vs low CP children (genome-wide significance; q<0.05)

| Probe | Gene | Chr | Genomic location | Position | *p*-value | q-value (FDR) | Direction | Early-onset CP Mean | Low CP Mean | % Diff | Cohen's *d* |
|---|---|---|---|---|---|---|---|---|---|---|---|
| cg12628061 | -- | 1 | -- | 56453730 | 2.47E-09 | 1.00E-03 | ↓ | 0.77 | 0.81 | 4% | 0.84 |
| cg02131674 | -- | 5 | -- | 17341065 | 1.64E-08 | 3.00E-03 | ↓ | 0.77 | 0.81 | 4% | 0.78 |
| cg15384400 | -- | 4 | -- | 36257279 | 5.09E-08 | 7.00E-03 | ↑ | 0.26 | 0.21 | 5% | 0.79 |
| cg07128473 | -- | 8 | -- | 116891579 | 1.00E-07 | 0.01 | ↓ | 0.83 | 0.86 | 3% | 0.76 |
| cg02503763 | *MGLL* | 3 | TSS1500 | 127542386 | 1.23E-07 | 0.01 | ↓ | 0.38 | 0.46 | 8% | 0.73 |
| cg21579239 | *TTBK2* | 15 | 5'UTR | 43211292 | 1.40E-07 | 0.01 | ↓ | 0.74 | 0.78 | 4% | 0.73 |
| cg16006965 | *GCET2* | 3 | TSS1500 | 111852325 | 7.85E-07 | 0.04 | ↓ | 0.53 | 0.6 | 7% | 0.66 |

[a] Arrows represent the direction of methylation differences, where ↑ indicates higher methylation levels in early-onset vs low CP children, while ↓ indicates lower methylation levels in early-onset vs low CP children. Cohen's *d*: .20 is a small effect size, .50 is a medium effect size, .80 is a large effect size.

**Table 2.** Candidate gene follow-up: Loci that differentiate between early-onset and low CP children (gene-level Bonferroni correction)

| Probe | Chr | Genomic Location | Position | *p*-value | q-value (genome-wide) | Bonferroni (gene-level) | Direction | Early-onset CP Mean | Low CP Mean | % Diff | Cohen's *d* |
|---|---|---|---|---|---|---|---|---|---|---|---|
| *BDNF* | | | | | | | | | | | |
| cg01225698 | 11 | Body; TSS1500 | 27742355 | 3.44E-04 | 0.30 | Significant | ↑ | 0.16 | 0.15 | 1% | 0.47 |
| cg18354203 | 11 | Body; 5'UTR | 27696004 | 4.97E-04 | 0.33 | Significant | ↓ | 0.72 | 0.75 | 3% | 0.49 |
| *FKBP5* | | | | | | | | | | | |
| cg07061368 | 6 | 5'UTR | 35631736 | 9.96E-04 | 0.37 | Significant | ↓ | 0.81 | 0.83 | 2% | 0.44 |
| *MAOA* | | | | | | | | | | | |
| cg05443523 | X | TSS200 | 43515213 | 1.17E-03 | 0.38 | Significant | ↑ | 0.36 | 0.33 | 3% | 0.44 |

*N.b.* Arrows represent the direction of methylation differences, where ↑ indicates higher methylation levels in early-onset vs low CP children, while ↓ indicates lower methylation levels in early-onset vs low CP children. Cohen's *d*: .20 is a small effect size, .50 is a medium effect size, .80 is a large effect size.

**Table 3.** Associations between prenatal environmental exposures and loci that are differentially methylated in early-onset vs low CP children.

| | ***Prenatal environment*** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Healthy diet | Unhealthy diet | Maternal smoking | Maternal alcohol use | Life events | Contextual risks | Parental risks | Interpersonal risks |
| ***Genome-wide analyses*** | | | | | | | | |
| cg12628061 | 0.09 | -0.06 | **-0.16 (*p* = 0.01)[a]** | **0.17 (*p* = 0.01)** | 0.09 | 0.02 | -0.09 | 0.07 |
| cg02131674 | 0.09 | -0.07 | -0.10 | 0.10 | 0.10 | 0.05 | -0.09 | 0.04 |
| cg15384400 | -0.07 | 0.07 | 0.09 | 0.00 | -0.05 | -0.01 | 0.11 | 0.05 |
| cg07128473 | **0.14 (*p* = 0.03)[a]** | -0.08 | -0.10 | 0.12 | 0.05 | 0.05 | -0.07 | 0.06 |
| cg02503763 (*MGLL*) | 0.03 | -0.01 | **-0.14 (*p* = 0.02)** | **0.13 (*p* = 0.03)[a]** | -0.05 | -0.04 | -0.08 | -0.02 |
| cg21579239 (*TTBK2*) | 0.08 | -0.07 | **-0.16 (*p* = 0.01)** | 0.09 | 0.09 | 0.04 | -0.12 | 0.02 |
| cg16006965 (*GCET2*) | 0.05 | 0.01 | -0.10 | **0.17 (*p* = 0.01)** | 0.07 | 0.09 | -0.07 | 0.04 |
| ***Candidate gene follow-up analyses*** | | | | | | | | |
| cg01225698 (*BDNF*) | -0.10 | 0.08 | 0.05 | -0.03 | -0.02 | 0.04 | 0.03 | 0.02 |
| cg18354203 (*BDNF*) | 0.06 | -0.12 | -0.09 | 0.00 | -0.01 | -0.03 | -0.06 | 0.07 |
| cg07061368 (*FKBP5*) | 0.00 | -0.03 | -0.08 | **0.20 (*p* = 0.001)[a]** | 0.11 | 0.08 | -0.03 | 0.10 |
| cg05443523 (*MAOA*) | -0.09 | 0.10 | 0.03 | -0.09 | **-0.13 (*p* = 0.001)[a]** | -0.02 | -0.01 | -0.04 |

*N.B.* All associations control for sex and cell-type. [a] Association remains significant after additionally controlling for other exposures, $p<0.05$

**Figure 1.** Methylomic variation at birth prospectively associated with early-onset vs low conduct problems in childhood

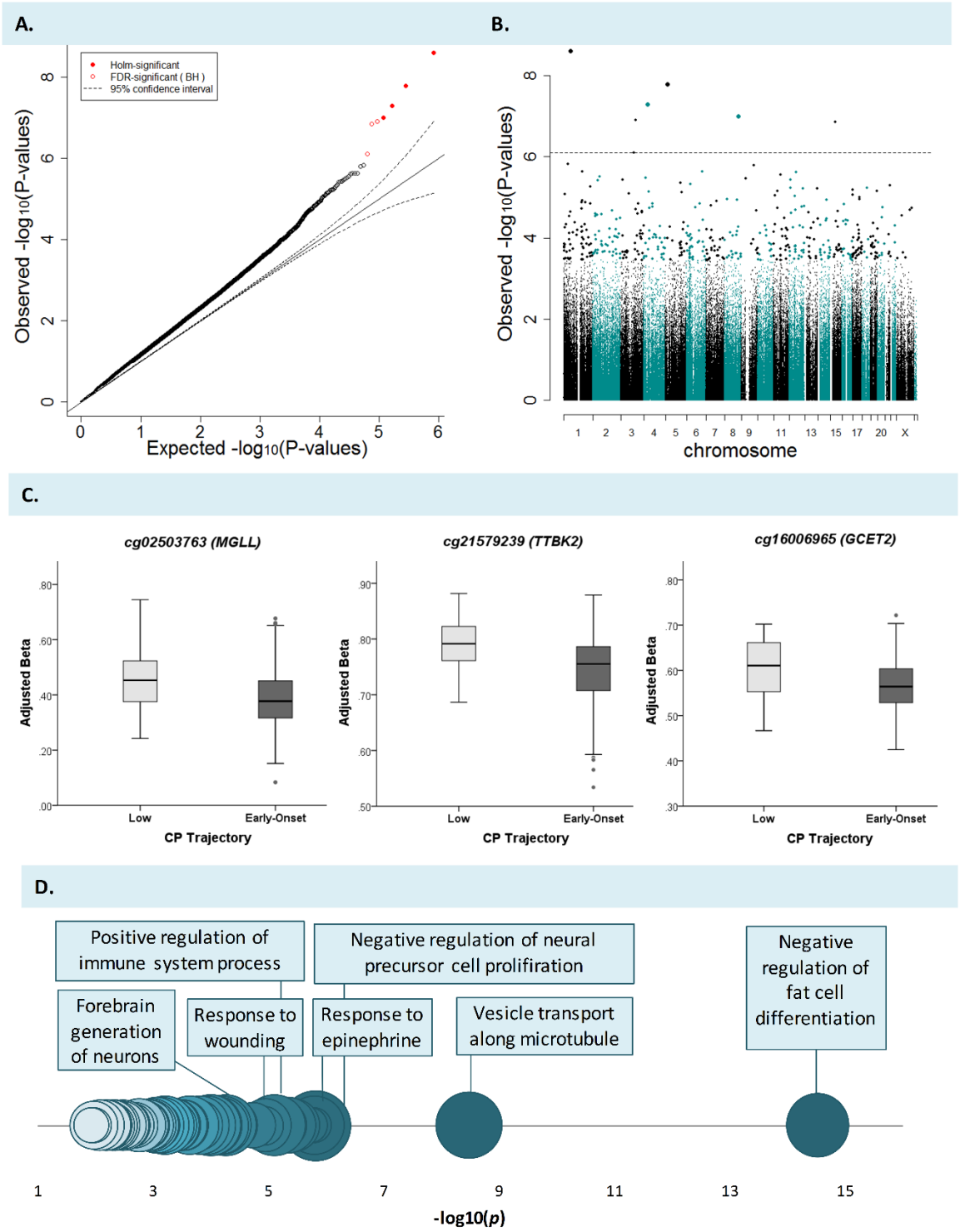
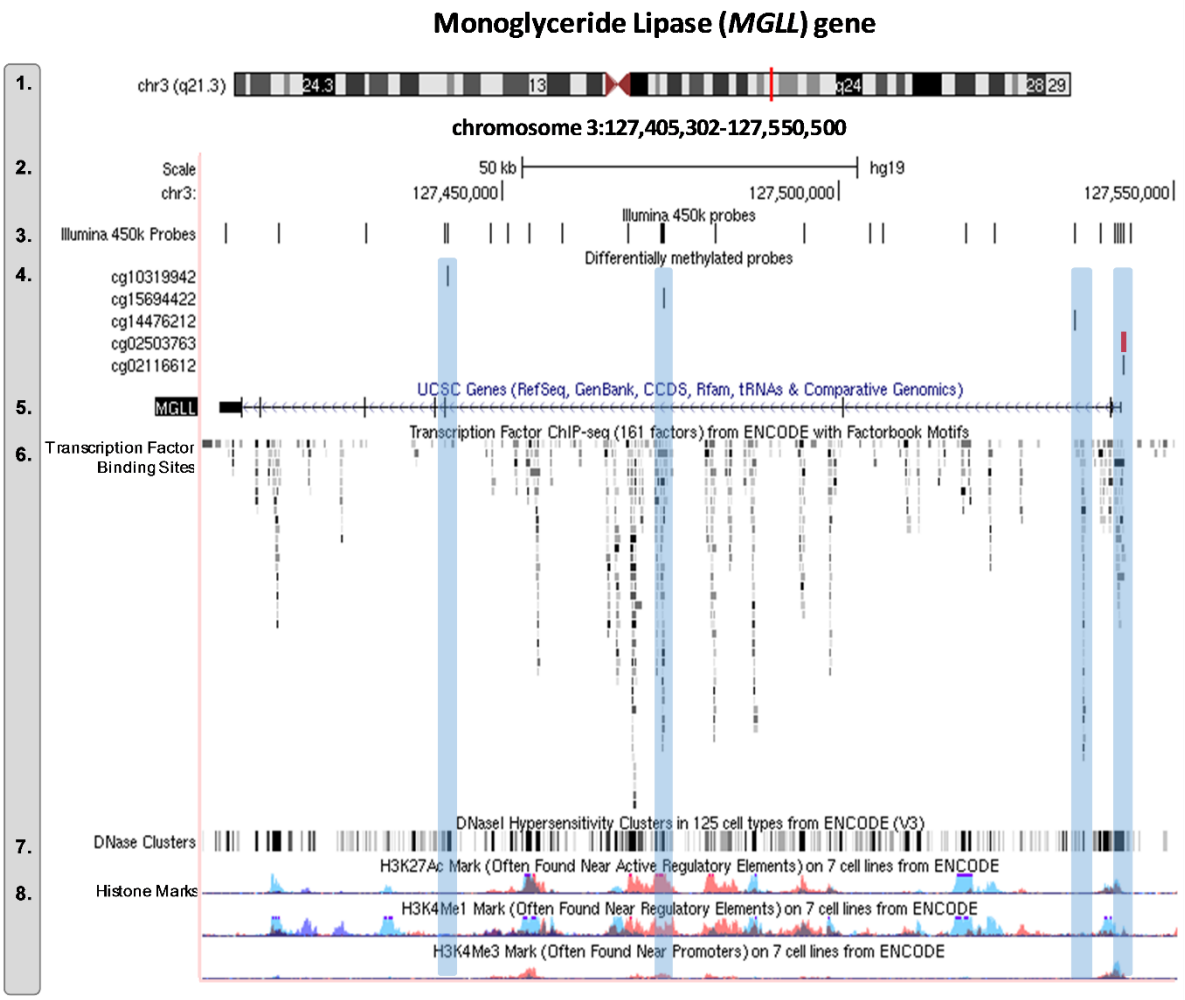


**Figure 2.** Functional characterization of *MGLL* DNA methylation sites associated with early-onset conduct problems



**Online Supplement**

*Neonatal DNA methylation and the emergence of early-onset conduct problems:*

*A genome-wide, prospective study*

**List of supplementary materials:**

**OS1.** List of items included in the prenatal cumulative adversity measures

**OS2.** Optimized gene ontology (GO) method.

**OS3**. Intercorrelations between DNAm levels across the identified sites

**OS4**. Boxplots of mean methylation differences between CP groups across four genome-wide significant probes ($q<0.05$) that are distal to annotated transcripts.

**OS5.** Top 20 enriched biological processes at birth differentiating early-onset vs low CP children based on GO pathway analysis

**OS6.** Detailed functional characterization of *MGLL* DNA methylation sites associated with early-onset conduct problems

**OS7** Candidate gene follow-up analyses

**OS8.** Comparison of DNAm levels across the identified loci between early-onset children who persist (i.e. EOP) vs desist (i.e. CL) in conduct problems over time.

**OS1.** List of items included in the prenatal cumulative adversity measures

| | *N. items* | *Range* | *M (SD)* | *Items* | |
|---|---|---|---|---|---|
| **Life events** | 22 | 0-8 | 2.48 (1.71) | Your partner died | You lost your job |
| | | | | One of your children died | You moved house |
| | | | | A friend or relative died | You were bleeding and thought you might miscarry |
| | | | | One of your children was ill | You started a new job |
| | | | | Your partner was ill | You had a test to see if your baby was abnormal |
| | | | | A friend or relative was ill | Result on a test that suggested your baby might not be normal |
| | | | | You were admitted to hospital | You were told that you were going to have twins |
| | | | | You were very ill | You heard something that happened might be harmful to the baby |
| | | | | Your partner lost his job | You took an examination |
| | | | | Your partner had problems at work | Your house or car was burgled |
| | | | | You had problems at work | You had an accident |
| **Contextual Risks** | 7 | 0-3 | .53 (.78) | You had a major financial problem | Housing adequacy |
| | | | | You became homeless | Housing Basic Living |
| | | | | Your income was reduced | Housing Defects |
| | | | | Financial difficulties | |
| **Parental Risks** | 9 | 0-5 | .51 (84) | You were in trouble with the law | Psychopathology of mother |
| | | | | Your partner was in trouble with the law | Substance abuse |
| | | | | You were convicted of an offence | Crime trouble with police |
| | | | | Early parenthood | Crime convictions |
| | | | | Maternal education | |
| **Interpersonal Risks** | 18 | 0-7 | 1.19 (1.41) | You were divorced | You found that your partner didn't want your child |
| | | | | Your partner went away | You argued with your partner |
| | | | | You and your partner separated | You had arguments with your family or friends |
| | | | | Partner Status | Your partner hurt you physically |
| | | | | Partner Affection | Your partner hurt your children physically |
| | | | | Partner Affection | Your partner hurt your children physically |
| | | | | Partner cruelty | Your partner was emotionally cruel to you |
| | | | | Family Size | Your partner was emotionally cruel to your children |
| | | | | Family Major problems | Social Network - Emotional |
| | | | | Partner Support | Social Network - Practical |

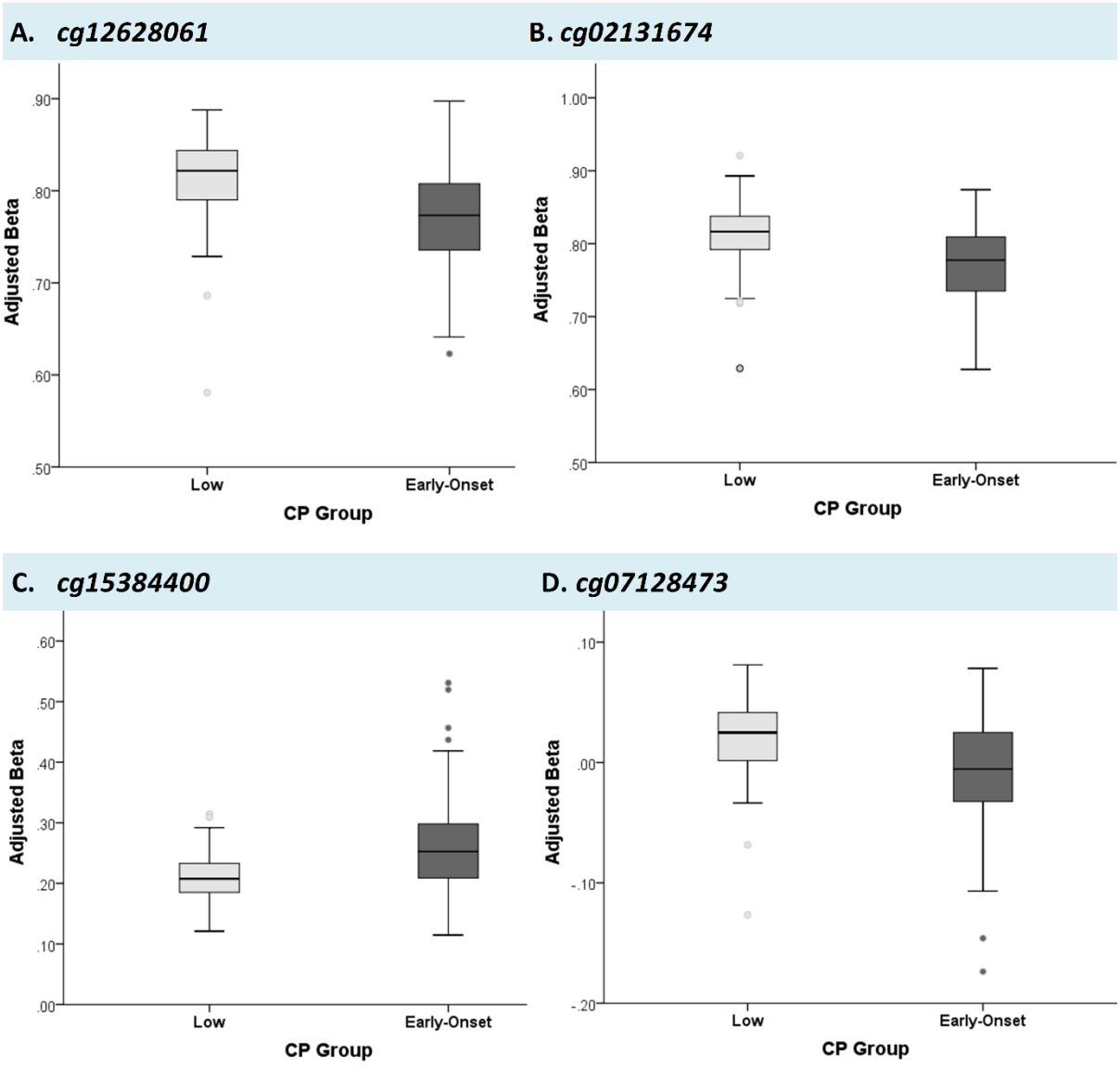
**OS2.** Optimized gene ontology method

A logistic regression approach was used to test if genes in the test list predicted pathway membership while controlling for the number probes annotated to each gene. Pathways were downloaded from the Gene Ontology website and all genes annotated to parent terms were also included. Illumina UCSC gene annotation was used to create a test gene list from probes that were associated with early-onset vs low conduct problems at birth ($p< 0.001$). All genes with at least one methylation probe annotated and annotated to at least one GO pathway were considered. Pathways were filtered to those with between 10 and 2000 genes in. After applying this method to all pathways, significant pathways ($p < 0.05$) were taken and grouped where overlapping genes explained the signal. This was achieved by taking the most significant pathway, and retesting all remaining significant pathways while controlling additionally for the best term. If genes in the test list no longer predicted the pathway, the term was said to be explained by the most significant pathway, and hence these pathways were grouped together. This algorithm was repeated, taking the next most significant term, until all pathways had been considered as the most significant or found to be explained by a more significant term. GO terms were interpreted exclusively if they if they contained at least 2 genes.

**OS3.** Intercorrelations between DNAm levels across the identified sites

| | | | Epigenome-wide analysis (genome-wide FDR correction) | | | | | | | Candidate gene follow-up analysis (gene-level bonferroni correction) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | cg12628061 | cg02131674 | cg15384400 | cg07128473 | cg02503763 *(MGLL)* | cg21579239 *(TTBK2)* | cg16006965 *(GCET2)* | cg01225698 *(BDNF)* | cg18354203 *(BDNF)* | cg07061368 *(FKBP5)* | cg05443523 *(MAOA)* |
| Epigenome-wide analysis | **cg12628061** | *r* | - | | | | | | | | | | |
| | | *p* | | | | | | | | | | | |
| | **cg02131674** | *r* | **0.57** | - | | | | | | | | | |
| | | *p* | 1.10E-28 | | | | | | | | | | |
| | **cg15384400** | *r* | **-0.21** | **-0.23** | - | | | | | | | | |
| | | *p* | 1.71E-04 | 4.07E-05 | | | | | | | | | |
| | **cg07128473** | *r* | **0.55** | **0.47** | **-0.52** | - | | | | | | | |
| | | *p* | 9.93E-27 | 5.63E-19 | 4.23E-23 | | | | | | | | |
| | **cg02503763 *(MGLL)*** | *r* | **0.20** | **0.24** | **-0.18** | **0.21** | - | | | | | | |
| | | *p* | 2.29E-04 | 2.01E-05 | 1.03E-03 | 1.37E-04 | | | | | | | |
| | **cg21579239 *(TTBK2)*** | *r* | **0.48** | **0.50** | **-0.24** | **0.37** | **0.22** | - | | | | | |
| | | *p* | 7.14E-20 | 3.09E-21 | 1.53E-05 | 1.56E-11 | 8.95E-05 | | | | | | |
| | **cg16006965 *(GCET2)*** | *r* | **0.42** | **0.33** | **-0.11** | **0.32** | **0.24** | **0.27** | - | | | | |
| | | *p* | 1.80E-15 | 1.46E-09 | 0.05 | 4.05E-09 | 1.46E-05 | 6.91E-07 | | | | | |
| Candidate gene follow-up analysis | **cg01225698 *(BDNF)*** | *r* | **-0.38** | **-0.31** | **0.23** | **-0.29** | **-0.09** | **-0.25** | **-0.16** | - | | | |
| | | *p* | 3.40E-12 | 1.13E-08 | 3.99E-05 | 7.74E-08 | 0.10 | 5.64E-06 | 3.41E-03 | | | | |
| | **cg18354203 *(BDNF)*** | *r* | **0.44** | **0.50** | **-0.07** | **0.41** | **0.20** | **0.43** | **0.23** | **-0.21** | - | | |
| | | *p* | 7.68E-17 | 9.05E-22 | 0.21 | 2.22E-14 | 3.62E-04 | 4.17E-16 | 2.56E-05 | 1.12E-04 | | | |
| | **cg07061368 *(FKBP5)*** | *r* | **0.47** | **0.44** | **-0.13** | **0.35** | **0.20** | **0.39** | **0.29** | **-0.17** | **0.36** | - | |
| | | *p* | 2.05E-19 | 1.72E-16 | 0.02 | 1.79E-10 | 4.33E-04 | 6.72E-13 | 2.03E-07 | 0.00 | 2.84E-11 | | |
| | **cg05443523 *(MAOA)*** | *r* | **-0.34** | **-0.26** | **0.28** | **-0.37** | **-0.14** | **-0.32** | **-0.10** | **0.27** | **-0.27** | **-0.16** | - |
| | | *p* | 2.93E-10 | 2.51E-06 | 4.36E-07 | 1.06E-11 | 0.01 | 7.80E-09 | 0.06 | 6.40E-07 | 6.90E-07 | 0.01 | |

**OS4.** Boxplots of mean methylation differences between CP groups across four genome-wide significant probes (q<0.05) that are distal to annotated transcripts.



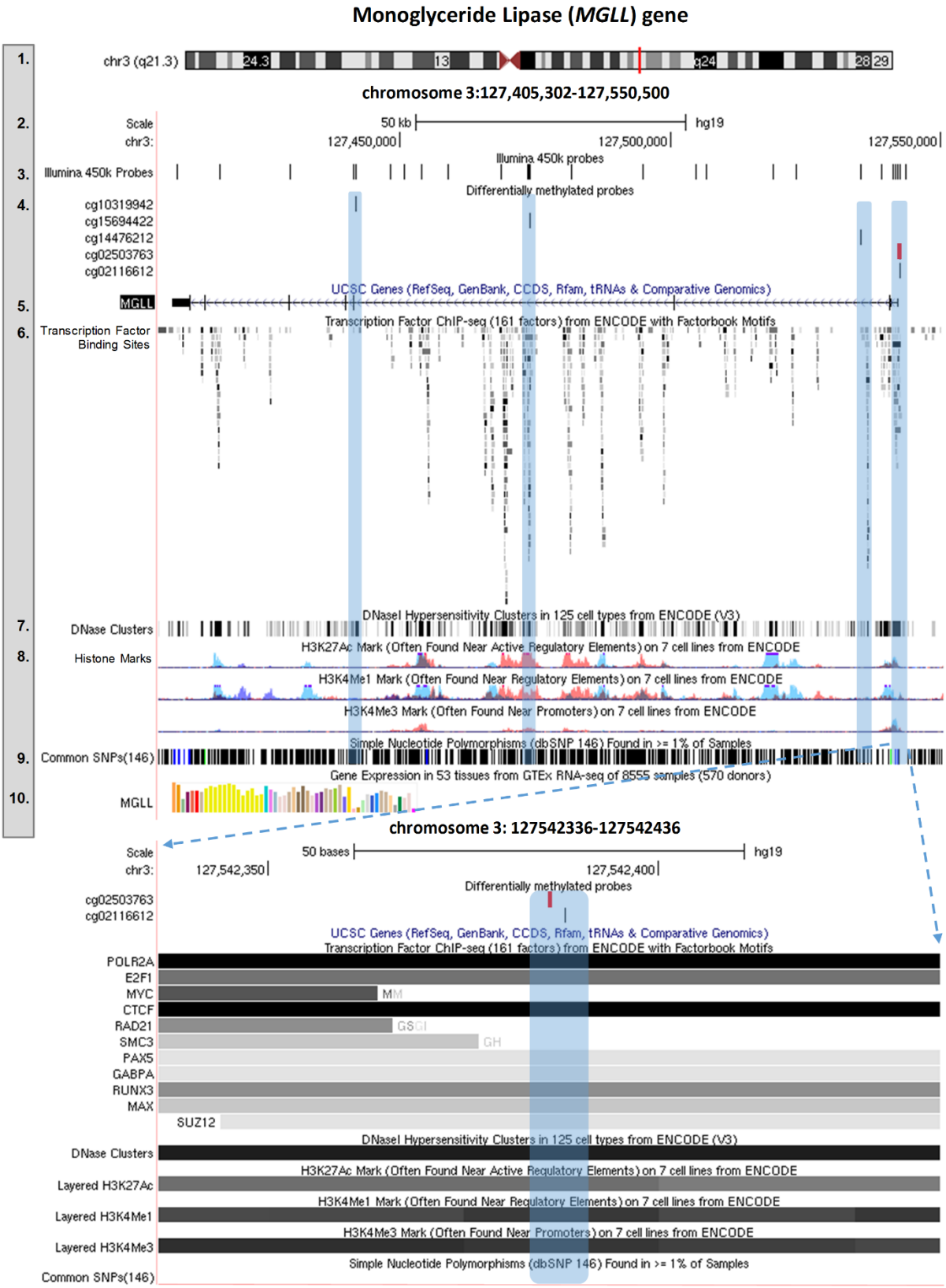
**OS5.** Top 20 enriched biological processes at birth differentiating early-onset vs low CP children based on GO pathway analysis

| | GO Pathway | *N* genes in study | Total *N* genes in pathway | % | *P*-value | Genes |
|---|---|---|---|---|---|---|
| 1 | Negative regulation of fat cell differentiation | 12 | 37 | 32.43% | 2.95E-15 | *WNT3A;GATA2;WWTR1;BBS12;ID4;SOD2;ZFPM2;TCF7L2;NCOR2;FOXO1;JDP2;ZFPM1* |
| 2 | Vesicle transport along microtubule | 6 | 17 | 35.29% | 3.33E-09 | *PRKCZ;FYCO1;HTT;KIF13A;NDE1;KIF3B* |
| 3 | Regulation of cell differentiation | 95 | 1186 | 8.01% | 6.93E-07 | *ITPKB;PRDM16;WNT3A;ARHGEF2;PRKCZ;TRIM11;RPS6KA1;DISC1;IL6R;TGFB2;CDC42;ID3;IGFBP5;CTNNA2;ZFP36L2;HDAC4;PAX8;CFLAR;CASP8;ZAP70;NCOA1;CTLA4;FNDC3B;FOXP1;TKT;GATA2;WWTR1;BCL6;ETV5;INPP4B;MSX1;TLR3;SFRP2;PROM1;PHOX2B;HTT;RAPGEF2;BBS12;GHR;C5orf13;ZSWIM6;OTP;MEGF10;TFAP2B;NR2E1;TFAP2A;ID4;PRDM1;NOTCH4;SOX4;SOD2;MAPK14;GLI3;INHBA;HDAC9;LIMK1;ASB4;LRRC17;HGF;ZFPM2;GDF6;PLAG1;TRPS1;MYST3;TCF7L2;VAX1;FGFR2;BMPR1A;IL15RA;BDNF;HCCA2;BAD;NCOR2;FGF23;SSH1;WIF1;PTPN6;STK24;FOXO1;JDP2;RGS6;RCOR1;NKX2-1;NEDD4;GREM1;ZFPM1;MED24;HOXB8;DCC;PRMT1;PRKACA;HPN;ZBTB46;OLIG2;RBM9* |
| 4 | Negative regulation of neural precursor cell proliferation | 5 | 17 | 29.41% | 1.47E-06 | *GATA2;HTT;NR2E1;VAX1;BDNF* |
| 5 | Response to epinephrine | 4 | 10 | 40.00% | 1.48E-06 | *PDE4B;PDE4D;RNLS;PRKACA* |
| 6 | Response to superoxide | 4 | 14 | 28.57% | 1.56E-06 | *PRDX1;SOD2;ERCC6;MPO* |
| 7 | Negative regulation of cell differentiation | 48 | 487 | 9.86% | 1.58E-06 | *PRDM16;WNT3A;ARHGEF2;TRIM11;ID3;IGFBP5;ZFP36L2;HDAC4;CTLA4;FOXP1;GATA2;WWTR1;BCL6;INPP4B;MSX1;TLR3;SFRP2;PHOX2B;HTT;RAPGEF2;BBS12;NR2E1;ID4;NOTCH4;SOX4;SOD2;GLI3;INHBA;LRRC17;ZFPM2;MYST3;TCF7L2;VAX1;BMPR1A;BDNF;NCOR2;FGF23;FOXO1;JDP2;NKX2-1;ZFPM1;MED24;HOXB8;DCC;PRMT1;HPN;ZBTB46;OLIG2* |
| 8 | Hemopoiesis | 41 | 431 | 9.51% | 1.86E-06 | *HIPK1;ITPKB;MFAP2;PRG4;WNT3A;PIK3CD;TGFB2;CDC42;CASP9;CD1D;SPTA1;IFI16;TPO;ZFP36L2;HDAC4;CASP8;ZAP70;TTC7A;MECOM;FOXP1;GATA2;BCL6;SFRP2;TXK;NOTCH4;SOX4;SOD2;MAPK14;GLI3;INHBA;HDAC9;ZFAT;ASH2L;TPD52;ANGPT1;MYST3;FGFR2;RCOR1;IREB2;CBFA2T3;ZFPM1* |
| 9 | Negative regulation of myeloid leukocyte differentiation | 8 | 35 | 22.86% | 3.73E-06 | *PRDM16;GATA2;INPP4B;TLR3;INHBA;LRRC17;ZFPM1;ZBTB46* |
| 10 | Regulation of macrophage differentiation | 5 | 20 | 25.00% | 4.47E-06 | *CASP8;GATA2;INHBA;PRKACA;ZBTB46* |
| 11 | Neutrophil migration | 7 | 37 | 18.92% | 5.48E-06 | *PDE4B;PIK3CD;TGFB2;FCER1G;PDE4D;PRKACA;ITGB2* |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | Positive regulation of immune system process | 49 | 626 | 7.83% | 5.89E-06 | *ITPKB;PDE4B;WNT3A;PRKCZ;PIK3CD;RPS6KA1;IL6R;TGFB2;CDC42;CD1D;MAPKAPK2;FCER1G;SPTA1;IFI16;WIPF1;CASP8;ZAP70;IGFBP2;CTLA4;FOXP1;BCL6;NCKIPSD;TLR3;EDNRA;CXCL13;TXK;PDE4D;RPS6KA2;C6orf150;PRDM1;MAPK14;ELMO1;GLI3;LIMK1;TRIL;IL15RA;IGF2;CD5;BAD;CADM1;BIRC3;IRAK4;PTPN6;C3AR1;THBS1;PRKCB;GRB2;ELANE;ITGB2* |
| 13 | Response to wounding | 74 | 1022 | 7.24% | 6.70E-06 | *WNT3A;PRKCZ;GNAI3;PIK3CD;CNR2;IL6R;TGFB2;CDC42;ID3;MAPKAPK2;PLA2G4A;FCER1G;IFI16;HDAC4;RAPGEF4;CFLAR;FN1;IL18RAP;MECOM;GP5;MGLL;GATA2;ATP2B2;DGKG;BCL6;CXCR6;TLR3;CNO;CXCL13;ARHGAP24;C5orf13;DST;DSP;SOD2;MAPK14;HIST1H3D;PRKAR1B;GLI3;HDAC9;TRIL;HGF;ZFPM2;PGCP;ANGPT1;KCNMA1;ALOX5;HPS6;SYT7;IGF2;BDNF;KRAS;CBX5;PTPN6;C3AR1;RACGAP1;SLC8A3;RCOR1;ITPK1;SLC7A7;THBS1;ZFPM1;PRKCB;GRB2;RPS6KB1;RAD51C;CCL16;CABLES1;PRKACA;GNA15;ELANE;PLAUR;KIF3B;IL10RB;ITGB2* |
| 14 | Retina layer formation | 4 | 13 | 30.77% | 7.84E-06 | *HIPK1;PROM1;TFAP2B;TFAP2A* |
| 15 | Regulation of gastrulation | 6 | 27 | 22.22% | 1.12E-05 | *WNT3A;SFRP2;OSR2;BMPR1A;OTX2;MAP2K5* |
| 16 | Regulation of ossification | 21 | 172 | 12.21% | 1.17E-05 | *IL6R;MATN1;TGFB2;ID3;IGFBP5;HDAC4;TKT;SFRP2;TFAP2A;ID4;GLI3;HGF;OSR2;EGR2;FGFR2;BMPR1A;CREB3L1;FGF23;MGP;GREM1;PRKACA* |
| 17 | Forebrain generation of neurons | 10 | 60 | 16.67% | 1.81E-05 | *WNT3A;RAPGEF2;OTP;NR2E1;TFAP2A;GLI3;LHX6;FGFR2;LHX5;NKX2-1* |
| 18 | Immune system process | 113 | 1842 | 6.13% | 3.81E-05 | *HIPK1;ITPKB;MFAP2;PDE4B;PRG4;WNT3A;ARHGEF2;CD1C;TRIM11;PIK3CD;RPS6KA1;SNX27;CNR2;IL6R;TGFB2;YTHDF2;CDC42;CASP9;PRDX1;CD1D;MAPKAPK2;FCER1G;SPTA1;ILF2;IFI16;TPO;ZFP36L2;HDAC4;WIPF1;CASP8;ZAP70;TTC7A;FN1;IL18RAP;CTLA4;MECOM;FOXP1;GATA2;BCL6;ST6GAL1;NCKIPSD;UBA7;TLR3;PITX2;SFRP2;CXCL13;TXK;PDE4D;NRG2;RPS6KA2;TAPBP;GNL1;C6orf150;PSMB8;HLA-DMB;NOTCH4;SOX4;SOD2;RNF8;MAPK14;ELMO1;PRKAR1B;GLI3;INHBA;HDAC9;LIMK1;TRIL;LRRC17;ZFAT;EIF2C2;ASH2L;TPD52;ANGPT1;MYST3;PSMB7;FGFR2;BMPR1A;CD5;BAD;IL18BP;MRE11A;BIRC3;PAN2;FGF23;KRAS;IRAK4;OAS3;PTPN6;C3AR1;RACGAP1;FLT1;FOXO1;RCOR1;SLC7A7;THBS1;SMAD6;IREB2;NEDD4;CBFA2T3;ZFPM1;PHLPP2;PRKCB;GRB2;MPO;CCL16;RPL13A;PRKACA;ELANE;KIF3B;CST7;IL10RB;ITGB2;POLR3H* |
| 19 | Regulation of protein export from nucleus | 5 | 24 | 20.83% | 4.23E-05 | *XPO1;HTT;SOX4;TCF7L2;PRKACA* |
| 20 | Cell differentiation in spinal cord | 9 | 53 | 16.98% | 4.64E-05 | *WNT3A;LHX4;IFT172;GATA2;SOX4;GLI3;DBX1;LHX5;OLIG2* |

*N.b.* GO pathways highlighted in orange are visually depicted in **Figure 1D** of the article.

**OS6.** Detailed functional characterization of *MGLL* DNA methylation sites associated with early-onset conduct problems



Expanded views from the UCSC genome browser of the *MGLL* gene showing the position of the DNAm sites associated with early-onset CP relative to ENCODE regulatory elements. The *top panel* shows functional characterization of the entire *MGLL* gene. Track numbers are displayed on the left-hand site, and represent the following **(1)** genomic positon of *MGLL* in chromosome 3; **(2)** genomic coordinates and scale; **(3)** location of all Illumina 450k probes that map onto the *MGLL* gene ($n$ = 26); **(4)** location of differentially methylated probes associated with early-onset vs low conduct problems ($n$ = 5). These are highlighted in blue to facilitate comparison with the regulatory elements displayed in lower tracks (track 6-8). In red is the probe that survived genome-wide correction ($MGLL_{cg02503763}$; all other probes significant at $p$<0.05); **(5)** schematic representation of the *MGLL* gene; **(6)** location of transcription factors (based on ChIP-seq data from 91 cell types), where darker shades indicate a stronger signal occupancy; **(7)** DNaseI hypersensitivity clusters (based on ChIP-seq data from 125 cell types), where darker shades also indicate a stronger signal; **(8)** levels of enrichment of three histone marks (H3K27Ac, H3K4Me1, and H3K4Me3) across three cell-types, including blood (GM12878 [red], K562 [purple]) and umbilical vein endothelial (HUVEC [blue]) cells; **(9)** location of common single-nucleotide polymorphisms (SNPs); and **(10)** median levels of *MGLL* expression across 51 tissues, based on RNA-seq data from the NIH Genotype-Tissue Expression (GTEx) project (midpoint milestone data release (V6, October 2015). Each bar represents a tissue, and the height of the bar indicates level of expression. Of note, yellow bars represent expression levels in brain tissue across multiple regions. These tracks are shown again in the *lower panel* of the figure, but this time specifically within the promoter region of *MGLL*, where our genome-wide significant DNAm site (in red) was located. Here, specific transcription factors binding to these regions are also shown.

**OS7.** Candidate gene follow-up analyses

| Gene name | Chr | Total *N* probes | Probes significant at p<0.05 (uncorrected) | | Gene-level significant (Bonferroni-corrected) | |
|---|---|---|---|---|---|---|
| | | | ***N*** | ***ProbeID*** | ***N*** | ***ProbeID*** |
| *Dopaminergic pathway* | | | | | | |
| *COMT* | 22 | 30 | 3 | cg03724721, cg08289189, cg21919834 | -- | -- |
| *DRD2* | 11 | 22 | 3 | cg12758687, cg14809166, cg18248586 | -- | -- |
| *DRD4* | 11 | 21 | 1 | cg08726248 | -- | -- |
| *MAOA* | X | 14 | 2 | cg05443523, cg18138788 | 1 | cg05443523 (↑) |
| *SLC6A3* | 5 | 52 | 3 | cg14502484, cg16703956, cg19440506 | -- | -- |
| *Serotonergic pathway* | | | | | | |
| *HTR1A* | 5 | 14 | 2 | cg11615755, cg13666507 | -- | -- |
| *HTR2A* | 13 | 25 | 6 | cg02027079, cg06476131, cg09361691, cg14059288**,** cg16188532, cg20102280 | -- | -- |
| *SLC6A4* | 17 | 14 | 2 | cg12074493, cg25725890 | -- | -- |
| *TPH1* | 11 | 4 | 1 | cg08400935 | -- | -- |
| *TPH2* | 12 | 18 | 2 | cg12017635, cg19530293 | -- | -- |
| *Neuroendocrine and neurodevelopmental pathway* | | | | | | |
| *AVP* | 20 | 14 | 1 | cg11491381 | -- | -- |
| *BDNF* | 11 | 73 | 8 | cg01225698, cg01418645, cg02527472, cg03747251, cg07159484, cg18354203, cg20954537, cg25412831 | 2 | cg01225698 (↑), cg18354203 (↓) |
| *FKBP5* | 6 | 32 | 4 | cg01294490, cg03546163, cg03591753, cg07061368 | 1 | cg07061368 (↓) |
| *NR3C1* | 5 | 35 | 7 | cg03857453, cg08818984, cg10847032,cg13648501, cg14558428, cg17860381, cg27122725 | -- | -- |
| *OXTR* | 3 | 17 | 1 | cg19619174 | -- | -- |

**OS8.** Comparison of DNAm levels across the identified loci between early-onset children who persist (i.e. EOP) vs desist (i.e. CL) in conduct problems over time

| | **Early-Onset CP children (*n* = 174)** | | | | **F** | ***p*** |
|---|---|---|---|---|---|---|
| | **CL trajectory (*n* = 83)** | | **EOP trajectory (*n*= 91)** | | | |
| | Mean | *Std. Dev.* | Mean | *Std. Dev.* | | |
| ***Genome-wide analyses*** | | | | | | |
| cg12628061 | 0.77 | *0.06* | 0.77 | *0.05* | 0.24 | 0.62 |
| cg02131674 | 0.77 | *0.06* | 0.77 | *0.05* | 0.15 | 0.70 |
| cg15384400 | 0.27 | *0.07* | 0.25 | *0.08* | 2.00 | 0.16 |
| cg07128473 | 0.83 | *0.04* | 0.84 | *0.04* | 0.46 | 0.50 |
| cg02503763 (*MGLL*) | 0.38 | *0.11* | 0.38 | *0.10* | 0.00 | 0.99 |
| cg21579239 (*TTBK2*) | 0.74 | *0.07* | 0.75 | *0.06* | 0.13 | 0.72 |
| cg16006965 (*GCET2*) | 0.57 | *0.06* | 0.56 | *0.06* | 3.11 | 0.08 |
| ***Candidate gene follow-up analyses*** | | | | | | |
| cg01225698 (*BDNF*) | 0.16 | *0.04* | 0.17 | *0.04* | 1.32 | 0.25 |
| cg18354203 (*BDNF*) | 0.71 | *0.07* | 0.72 | *0.07* | 0.74 | 0.39 |
| cg07061368 (*FKBP5*) | 0.81 | *0.06* | 0.81 | *0.04* | 0.87 | 0.35 |
| cg05443523 (*MAOA*) | 0.37 | *0.06* | 0.35 | *0.05* | 1.57 | 0.21 |